



8

SEQUENCE LISTING

<110> HYBRIGENICS

Pierre, Legrain

<120> Protein-protein interactions in adipocyte cells

<130> B4767A

<140> US 10/038,010

<141> 2002-01-02

<150> US 60/259,377

<151> 2001-01-02

<160> 67

<170> PatentIn version 3.1

<210> 1

<211> 492

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(492)

<223> Human Skp1 : Part of SCF (Skp1/Cullin/F-box) complexes which act as E3 Ubiquitin ligases.

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60

gccaaacaat	ctgtaactat	taagaccatg	ttggaagatt	tgggaatgga	tgatgaagga	120
gatgatgacc	cagttcctct	accaaattgt	aatgcagcaa	tattaaaaaa	ggcattcag	180
tgggtgcacc	accacaagga	tgaccctcct	cctcctgaag	atgatgagaa	caaagaaaag	240
cggacagatg	atatccctgt	ttgggaccaa	gaattcctga	aagttgacca	aggaacactt	300
tttgaactca	ttctggctgc	aaactactta	gacatcaaag	gtttgcttga	tgttacatgc	360
aagactgttg	ccaatatgat	caaggggaaa	actcctgagg	agattcgcaa	gaccttcaat	420
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gaagagaagt	ga					492

 $\langle 210 \rangle \quad 2$

<211> 163

<212> PRT

<213> Homo sapiens

<220>

<221> Skp1

<222> (1) .. (163)

<223>

<400> 2

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Asp Val Glu Ile Ala Lys Gln Ser Val Thr Ile Lys Thr Met Leu Glu
20 25 30

Asp Leu Gly Met Asp Asp Glu Gly Asp Asp Asp Pro Val Pro Leu Pro
35 40 45

Asn Val Asn Ala Ala Ile Leu Lys Lys Val Ile Gln Trp Cys Thr His
50 55 60

His Lys Asp Asp Pro Pro Pro Pro Glu Asp Asp Glu Asn Lys Glu Lys
65 70 75 80

Arg Thr Asp Asp Ile Pro Val Trp Asp Gln Glu Phe Leu Lys Val Asp

	85		90		95
Gln Gly Thr	Leu Phe Glu Leu Ile	Leu Ala Ala Asn Tyr	Leu Asp Ile		
	100	105	110		
Lys Gly Leu	Leu Asp Val Thr Cys Lys	Thr Val Ala Asn Met	Ile Lys		
	115	120	125		
Gly Lys Thr	Pro Glu Glu Ile Arg Lys	Thr Phe Asn Ile	Lys Asn Asp		
	130	135	140		
Phe Thr Glu	Glu Glu Glu Ala Gln Val	Arg Lys Glu Asn	Gln Trp Cys		
	145	150	155	160	
Glu Glu Lys					

<210> 3

<211> 1917

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (1917)

<223> Human Splicing Factor 1

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ccccctggac ttactcgaga acaagaaaga gcttatatag tgcaactgca gatagaagac	180
ctgactcgta aactgcgcac aggagacctg ggcattcccc ctaaccctga ggacaggtcc	240
ccttccccctg agcccatcta caatagcgag gggaagcggc ttaacacccg agagttccgc	300
acccgcaaaa agctggaaga ggagcggcac aacctcatca cagagatggt tgcactcaat	360
ccggatttca agccacctgc agattacaaa cctccagcaa cacgtgtgag tgataaagtc	420
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gggaacaccc tgaagaacat agagaaggag tgcaatgcc aagattatgat ccgggggaaa	540

gggtctctgtga	aagaaggaggaa	ggttggggcgc	aaagatggcc	agatgttgcc	aggagaagat	600
gagccacttc	atgccctggt	tactgccaat	acaatggaga	acgtcaaaaa	ggcagtggaa	660
cagataagaa	acatcctgaa	gcaggggtatc	gagactccag	aggaccagaa	tgatctacgg	720
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atcttaagac	cctggcagag	ctcagagacc	cgcagcatta	ccaacaccac	agtgtgtacc	840
aagtgtggag	gggctggcca	cattgcttca	gactgtaaat	tccaaaggcc	tggtgatcct	900
cagtcagctc	aggataaagc	acggatggat	aaagaatatt	tgtccctcat	ggctgaactg	960
ggtgaagcac	ctgtcccagc	atctgtgggc	tccacctctg	ggcctgccac	cacaccctg	1020
gccagcgcac	ctcgtcctgc	tgtcccgcc	aacaaccac	ctccaccgtc	tctcatgtct	1080
accaccacaga	gccgcccacc	ctggatgaat	tctggccctt	cagagagtcg	gccctaccac	1140
ggcatgcatg	gaggtggtc	tggtggggcc	ggaggtggcc	cccacagctt	cccacacca	1200
ttaccacagc	tgacaggtgg	gcatggtgga	catcccatgc	agcacaacc	caatggacce	1260
ccaccctt	ggatgcagcc	accaccacca	ccgatgaacc	agggcccca	ccctcctggg	1320
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accccttgc	catggcagca	aaatacgacg	actaccacca	cgagcgtgg	cacaggtcc	1620
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ggcggcgatg	gcccagacca	tgagagtgag	gactttccgc	gccattgg	gacccttcca	1860
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<220>

<221> Human Splicing Factor 1

<222> (1)..(638)

<223>

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Ile Pro Gly Met Pro Thr Val Ile Pro Pro Gly Leu Thr Arg Glu Gln
35 40 45

Glu Arg Ala Tyr Ile Val Gln Leu Gln Ile Glu Asp Leu Thr Arg Lys
50 55 60

Leu Arg Thr Gly Asp Leu Gly Ile Pro Pro Asn Pro Glu Asp Arg Ser
65 70 75 80

Pro Ser Pro Glu Pro Ile Tyr Asn Ser Glu Gly Lys Arg Leu Asn Thr
85 90 95

Arg Glu Phe Arg Thr Arg Lys Lys Leu Glu Glu Glu Arg His Asn Leu
100 105 110

Ile Thr Glu Met Val Ala Leu Asn Pro Asp Phe Lys Pro Pro Ala Asp
115 120 125

Tyr Lys Pro Pro Ala Thr Arg Val Ser Asp Lys Val Met Ile Pro Gln
130 135 140

Asp Glu Tyr Pro Glu Ile Asn Phe Val Gly Leu Leu Ile Gly Pro Arg
145 150 155 160

Gly Asn Thr Leu Lys Asn Ile Glu Lys Glu Cys Asn Ala Lys Ile Met
165 170 175

Ile Arg Gly Lys Gly Ser Val Lys Glu Gly Lys Val Gly Arg Lys Asp
180 185 190

Gly Gln Met Leu Pro Gly Glu Asp Glu Pro Leu His Ala Leu Val Thr
195 200 205

[illegible]

Gln Tyr Leu Gly Ser Thr Pro Val Gly Ser Gly Val Tyr Arg Leu His
 450 455 460

Gln Gly Lys Gly Met Met Pro Pro Pro Pro Met Gly Met Met Pro Pro
 465 470 475 480

Pro Pro Pro Pro Pro Ser Gly Gln Pro Pro Pro Pro Pro Ser Gly Pro
 485 490 495

Leu Pro Pro Trp Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro
 500 505 510

Pro Ser Ser Ser Met Ala Ser Ser Thr Pro Leu Pro Trp Gln Gln Asn
 515 520 525

Thr Thr Thr Thr Thr Thr Ser Ala Gly Thr Gly Ser Ile Pro Pro Trp
 530 535 540

Gln Gln Gln Gln Ala Ala Ala Ala Ala Ser Pro Gly Ala Pro Gln Met
 545 550 555 560

Gln Gly Asn Pro Thr Met Val Pro Leu Pro Pro Gly Val Gln Pro Pro
 565 570 575

Leu Pro Pro Gly Ala Pro Pro Pro Pro Pro Pro Pro Pro Gly Ser
 580 585 590

Ala Gly Met Met Ile Pro Pro Arg Gly Gly Asp Gly Pro Ser His Glu
 595 600 605

Ser Glu Asp Phe Pro Arg Pro Leu Val Thr Leu Pro Gly Arg Gln Pro
 610 615 620

Gln Gln Arg Pro Trp Trp Thr Gly Trp Phe Gly Lys Ala Ala
 625 630 635

- <210> 5
- <211> 1173
- <212> DNA
- <213> mouse p53
- <220>

<221> gene

<222> (1)..(1173)

<223> mouse p53 : Tumour suppressor protein

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atggacgatac tgttgctgcc ccaggatgtt gaggagtttt ttgaaggccc aagtgaagcc 180
ctccgagtgt caggagctcc tgcagcacag gaccctgtca ccgagacccc tgggccagcg 240
gcccctgccc cagccactcc atggcccctg tcactttttg tcccttctca aaaaacttac 300
cagggcaact atggcttcca cctgggcttc ctgcagtctg ggacagccaa gtctgttatg 360
tgacagtact ctctccct caataagcta ttctgccagc tggcgaagac gtgccctgtg 420
cagttgtggg tcagcgccac acctccagct gggagccgtg tccgcgccat ggccatctac 480
aagaagtcac agcacatgac ggaggtcgtg agacgtgcc cccaccatga gcgctgctcc 540
gatggtgatg gcctggctcc tccccagcat cttatccggg tggaaggaaa tttgtatccc 600
gagtatctgg aagacaggca gacttttcgc cacagcgtgg tggtagctta tgagccaccc 660
gaggccggct ctgagtatac caccatccac tacaagtaca tgtgtaatag ctctgcatg 720
gggggcatga accgcccacc tacccttacc atcatcacac tggaagactc cagtgggaac 780
cttctgggac gggacagctt tgagggttcgt gtttgtgctt gccctgggag agaccgccgt 840
acagaagaag aaaatttccg caaaaaggaa gtccctttgcc ctgaactgcc cccagggagc 900
gcaaagagag cgctgcccac ctgcacaagc gcctctcccc cgcaaaagaa aaaaccactt 960
gatggagagt atttcacct caagatccgc gggcgtaaac gcttcgagat gttccgggag 1020
ctgaatgagg ccttagagtt aaaggatgcc catgctacag aggagtctgg agacagcagg 1080
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<210> 6

<211> 390

<212> PRT

<213> mouse p53

[illegible] $\langle 220 \rangle$

<221> p53

<222> (1) .. (390)

<223>

<400> 6

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Leu Ser Gln Glu Thr Phe Ser Gly Leu Trp Lys Leu Leu Pro Pro Glu
20 25 30

Asp Ile Leu Pro Ser Pro His Cys Met Asp Asp Leu Leu Leu Pro Gln
35 40 45

Asp Val Glu Glu Phe Phe Glu Gly Pro Ser Glu Ala Leu Arg Val Ser
50 55 60

Gly Ala Pro Ala Ala Gln Asp Pro Val Thr Glu Thr Pro Gly Pro Ala
65 70 75 80

Ala Pro Ala Pro Ala Thr Pro Trp Pro Leu Ser Ser Phe Val Pro Ser
85 90 95

Gln Lys Thr Tyr Gln Gly Asn Tyr Gly Phe His Leu Gly Phe Leu Gln
100 105 110

Ser Gly Thr Ala Lys Ser Val Met Cys Thr Tyr Ser Pro Pro Leu Asn
115 120 125

Lys Leu Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val
130 135 140

Ser Ala Thr Pro Pro Ala Gly Ser Arg Val Arg Ala Met Ala Ile Tyr
145 150 155 160

Lys Lys Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His
165 170 175

Glu Arg Cys Ser Asp Gly Asp Gly Leu Ala Pro Pro Gln His Leu Ile
180 185 190

Arg Val Glu Gly Asn Leu Tyr Pro Glu Tyr Leu Glu Asp Arg Gln Thr

195	200	205
Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Ala Gly Ser		
210	215	220
Glu Tyr Thr Thr Ile His Tyr Lys Tyr Met Cys Asn Ser Ser Cys Met		
225	230	235 240
Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp		
	245	250 255
Ser Ser Gly Asn Leu Leu Gly Arg Asp Ser Phe Glu Val Arg Val Cys		
	260	265 270
Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Phe Arg Lys		
	275	280 285
Lys Glu Val Leu Cys Pro Glu Leu Pro Pro Gly Ser Ala Lys Arg Ala		
	290	295 300
Leu Pro Thr Cys Thr Ser Ala Ser Pro Pro Gln Lys Lys Lys Pro Leu		
305	310	315 320
Asp Gly Glu Tyr Phe Thr Leu Lys Ile Arg Gly Arg Lys Arg Phe Glu		
	325	330 335
Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala His Ala		
	340	345 350
Thr Glu Glu Ser Gly Asp Ser Arg Ala His Ser Ser Tyr Leu Lys Thr		
	355	360 365
Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Thr Met Val Lys Lys		
	370	375 380
Val Gly Pro Asp Ser Asp		
385	390	

<210> 7

<211> 1710

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(1710)

<223> Human beta-TrCP1 : F-box containing protein with 7 WD40 repeats;
Part of SCF (Skp1/Cullin/F-box) complex E3 ubiquitin ligase; Impl
icated in the degradation of b-catenin and IkBa

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agacagacat acaacagctg tgccagactc tgcttaaacc aagaaacagt atgttttagca 180
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caagacattg agacaataga atctaattgg agatgtggaa gacatagttt acagagaatt 780
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<210> 8

<211> 569

<212> PRT

<213> Homo sapiens

<220>

<221> beta-TrCP1

<222> (1) .. (569)

<223>

<400> 8

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 20 25 30

Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
 35 40 45

Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
 50 55 60

Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
 65 70 75 80

Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
 85 90 95

Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
 100 105 110

Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
115 120 125

His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
130 135 140

Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
145 150 155 160

Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
165 170 175

Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
180 185 190

Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
195 200 205

Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
210 215 220

Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
225 230 235 240

Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
245 250 255

Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
260 265 270

Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
275 280 285

Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr
290 295 300

Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile
305 310 315 320

Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr
325 330 335

Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His
340 345 350

Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser

355		360		365
Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp	Ile Thr Leu Arg Arg			
370	375	380		
Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp				
385	390	395	400	
Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn				
	405	410	415	
Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly				
	420	425	430	
Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser				
435	440	445		
Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg				
450	455	460		
Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn				
465	470	475	480	
Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp				
	485	490	495	
Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu				
	500	505	510	
Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp				
	515	520	525	
Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp				
530	535	540		
Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro				
545	550	555	560	
Ser Arg Thr Tyr Thr Tyr Ile Ser Arg				
	565			

<210> 9

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(579)

<223> human Rac1 : Member of Ras subfamily of RAS small GTPases

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tctgccaatg ttatggtaga tggaaaaccg gtgaatctgg gcttatggga tacagctgga 180
caagaagatt atgacagatt acgcccccta tcctatccgc aaacagatgt gttcttaatt 240
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gatgataaag acacgatcga gaaactgaag gagaagaagc tgactcccat cacctatccg 420
caggggtctag ccatggctaa ggagattggg gctgtaaaat acctggagtg ctcggcgctc 480
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cccgtaaga agaggaagag aaaatgcctg ctgttgtaa 579

<210> 10

<211> 192

<212> PRT

<213> Homo sapiens

<220>

<221> Rac1

<222> (1)..(192)

<223>

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Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys
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.....

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20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Gly
35 40 45

Lys Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr
50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile
65 70 75 80

Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn Val Arg Ala Lys
85 90 95

Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Thr Pro Ile Ile Leu
100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys
115 120 125

Leu Lys Glu Lys Lys Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala
130 135 140

Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser Ala Leu
145 150 155 160

Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val
165 170 175

Leu Cys Pro Pro Pro Val Lys Lys Arg Lys Arg Lys Cys Leu Leu Leu
180 185 190

<210> 11
<211> 915
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1)..(915)

<223> Human uracil DNA glycosylase : Uracil DNA glycosylase implicated
in DNA repair

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aaggccccgg ctgggcagga ggagcctggg acgccgccct cctcgccgct gagtgccgag 180
cagttggacc ggatccagag gaacaaggcc gcggccctgc tcagactcgc ggcccgcaac 240
gtgcccgtgg gcttttgaga gagctggaag aagcacctca gcggggagtt cgggaaaccg 300
tattttatca agctaattggg atttgttgca gaagaaagaa agcattacac tgtttatcca 360
ccccacacc aagtcttcac ctggaccag atgtgtgaca taaaagatgt gaaggttgtc 420
atcctgggac aggatccata tcatggacct aatcaagctc acgggctctg ctttagtggt 480
caaaggcctg ttccgcctcc gccagtttg gagaacattt ataaagagtt gtctacagac 540
atagaggatt ttgttcatcc tggccatgga gatttatctg ggtgggcaa gcaagggtgt 600
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caccatgtac tacagacggc tcatccctcc ctttgtcag tgtatagagg gttctttgga 840
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tggaaggagc tgtga 915

<210> 12

<211> 304

<212> PRT

<213> Homo sapiens

<220>

<221> DNA glycosylase

<222> (1) .. (304)

<223>

<400> 12

Met Gly Val Phe Cys Leu Gly Pro Trp Gly Leu Gly Arg Lys Leu Arg
1 5 10 15

Thr Pro Gly Lys Gly Pro Leu Gln Leu Leu Ser Arg Leu Cys Gly Asp
20 25 30

His Leu Gln Ala Ile Pro Ala Lys Lys Ala Pro Ala Gly Gln Glu Glu
35 40 45

Pro Gly Thr Pro Pro Ser Ser Pro Leu Ser Ala Glu Gln Leu Asp Arg
50 55 60

Ile Gln Arg Asn Lys Ala Ala Ala Leu Leu Arg Leu Ala Ala Arg Asn
65 70 75 80

Val Pro Val Gly Phe Gly Glu Ser Trp Lys Lys His Leu Ser Gly Glu
85 90 95

Phe Gly Lys Pro Tyr Phe Ile Lys Leu Met Gly Phe Val Ala Glu Glu
100 105 110

Arg Lys His Tyr Thr Val Tyr Pro Pro Pro His Gln Val Phe Thr Trp
115 120 125

Thr Gln Met Cys Asp Ile Lys Asp Val Lys Val Val Ile Leu Gly Gln
130 135 140

Asp	Pro	Tyr	His	Gly	Pro	Asn	Gln	Ala	His	Gly	Leu	Cys	Phe	Ser	Val
145					150					155					160

Gln Arg Pro Val Pro Pro Pro Pro Ser Leu Glu Asn Ile Tyr Lys Glu
165 170 175

Leu Ser Thr Asp Ile Glu Asp Phe Val His Pro Gly His Gly Asp Leu
180 185 190

Ser Gly Trp Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr
195 200 205

Val	Arg	Ala	His	Gln	Ala	Asn	Ser	His	Lys	Glu	Arg	Gly	Trp	Glu	Gln
	210					215					220				

Phe Thr Asp Ala Val Val Ser Trp Leu Asn Gln Asn Ser Asn Gly Leu
225 230 235 240

Val Phe Leu Leu Trp Gly Ser Tyr Ala Gln Lys Lys Gly Ser Ala Ile

245 250 255

Asp Arg Lys Arg His His Val Leu Gln Thr Ala His Pro Ser Pro Leu
260 265 270

Ser Val Tyr Arg Gly Phe Phe Gly Cys Arg His Phe Ser Lys Thr Asn
275 280 285

Glu Leu Leu Gln Lys Ser Gly Lys Lys Pro Ile Asp Trp Lys Glu Leu
290 295 300

<210> 13

<211> 158

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(158)

<223> Human b2 adrenergic receptor : Oncogene

<400> 13
tcttttcagga ggccaaaagg cagctccaga agattgacaa atctgagggc cgcttccatg 60
tccagaacct tagccagggtg gagcaggatg ggcggacggg gcatggactc cgcagatctt 120
ccaagttctg cttgaaggag cacaaagccc tcaagtga 158

<210> 14

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> b2 adrenergic receptor

<222> (1)..(52)

<223>

<400> 14

Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu
1 5 10 15
Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg
20 25 30
Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His
35 40 45
Lys Ala Leu Lys
50

<210> 15

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(261)

<223> Human b2 adrenergic receptor : Oncogene

<400> 15
cggagcccag atttcaggat tgccttccag gagcttctgt gcctgcgag gtcttctttg 60
aaggcctatg gcaatggcta ctccagcaac ggcaacacag gggagcagag tggatatcac 120
gtggaacagg agaaagaaaa taaactgctg tgtgaagacc tcccaggcac ggaagacttt 180
gtgggccatc aaggtactgt gcctagcgat aacattgatt cacaaggag gaattgtagt 240
acaaatgact cactgctata a 261

<210> 16

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> b2 adrenergic receptor

<222> (1)..(86)

<223>

<400> 16

Arg Ser Pro Asp Phe Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg
1 5 10 15

Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn
20 25 30

Thr Gly Glu Gln Ser Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys
35 40 45

Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln
50 55 60

Gly Thr Val Pro Ser Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser
65 70 75 80

Thr Asn Asp Ser Leu Leu
85

<210> 17

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(423)

<223> Human b2 adrenergic receptor : Oncogene

<400> 17

gtcttttcagg aggccaaaag gcagctccag aagattgaca aatctgaggg ccgcttccat 60

gtccagaacc ttagccaggt ggagcaggat gggcggacgg ggcattggact ccgcagatct 120
 tccaagttct gcttgaagga gcacaaagcc ctcaagggat cccggagccc agatttcagg 180
 attgccttcc aggagcttct gtgcctgctc aggtcttctt tgaaggccta tggcaatggc 240
 tactccagca acggcaacac aggggagcag agtggatatc acgtggaaca ggagaaagaa 300
 aataaactgc tgtgtgaaga cctcccaggc acggaagact ttgtgggcca tcaagggtact 360
 gtgcctagcg ataacattga ttcacaaggg aggaattgta gtacaaatga ctactgcta 420
 taa 423

<210> 18

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> b2 adrenergic receptor

<222> (1)..(140)

<223>

<400> 18

Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu
 1 5 10 15

Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg
 20 25 30

Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His
 35 40 45

Lys Ala Leu Lys Gly Ser Arg Ser Pro Asp Phe Arg Ile Ala Phe Gln
 50 55 60

Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly
 65 70 75 80

Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val Glu
 85 90 95

Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu
 100 105 110

Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp Ser
 115 120 125

Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
 130 135 140

<210> 19

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (579)

<223> Human b2 adrenergic receptor : Oncogene

<400> 19
 gtcttttcagg aggccaaaag gcagctccag aagattgaca aatctgaggg ccgcttccat 60
 gtccagaacc ttagccaggt ggagcaggat gggcggacgg ggcattggact ccgcagatct 120
 tccaagttct gcttgaagga gcacaaagcc ctcaagacgt taggcatcat catgggcact 180
 ttcaccctct gctggctgcc cttcttcata gttaacattg tgcattgtgat ccaggataac 240
 ctcatccgta aggaagttta catcctccta aattggatag gctatgtcaa ttctgggttc 300
 aatcccctta tctactgccg gagcccagat ttcaggattg ccttccagga gcttctgtgc 360
 ctgctgcagg tttctttgaa ggcctatggc aatggctact ccagcaacgg caacacaggg 420
 gagcagagtg gatattcacgt ggaacaggag aaagaaaata aactgctgtg tgaagacctc 480
 ccaggcacgg aagactttgt gggccatcaa ggtactgtgc ctagcgataa cattgattca 540
 caagggagga attgtagtac aaatgactca ctgctataa 579

<210> 20

<211> 192

<212> PRT

<213> Homo sapiens

<220>

<221> b2 adrenergic receptor

<222> (1)..(192)

<223>

<400> 20

Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu
1 5 10 15

Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg
20 25 30

Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His
35 40 45

Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys
50 55 60

Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn
65 70 75 80

Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val
85 90 95

Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg
100 105 110

Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala
115 120 125

Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly
130 135 140

Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu
145 150 155 160

Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp
165 170 175

Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu


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180
185
190

<210> 21
<211> 1794
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1) .. (1794)
<223> hSHP2_FL

<400> 21
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ttgacaagag gagttaatgg cagttttttg gcaaggccta gtaaaagtaa ccctgggagac      120
ttcacacttt ccgttagaag aaatggagct gtcaccaca tcaagattca gaacactggt      180
gattactatg acctgtatgg aggggagaaa tttgccactt tggctgagtt ggtccagtat      240
tacatggaac atcacgggca attaaaagag aagaatggag atgtcattga gcttaaatat      300
cctctgaact gtgcagatcc tacctctgaa aggtggtttc atggacatct ctctgggaaa      360
gaagcagaga aattattaac tgaaaaagga aaacatggta gttttcttgt acgagagagc      420
cagagccacc ctggagattt tgttctttct gtgcgcactg gtgatgacaa aggggagagc      480
aatgacggca agtctaaagt gacctatggt atgattcgct gtcaggaact gaaatacgac      540
gttggtggag gagaacgggt tgattctttg acagatcttg tggaacatta taagaagaat      600
cctatggtgg aaacattggg tacagtacta caactcaagc agccccttaa cacgactcgt      660
ataaatgctg ctgaaataga aagcagagtt cgagaactaa gcaaattagc tgagaccaca      720
gataaagtca aacaaggctt ttgggaagaa tttgagacac tacaacaaca ggagtgcaaa      780
cttctctaca gccgaaaaga ggggtcaaagg caagaaaaca aaaacaaaaa tagatataaa      840
aacatcctgc cctttgatca taccaggggt gtccacacg atggtgatcc caatgagcct      900
gtttcagatt acatcaatgc aaatatcatc atgcctgaat ttgaaaccaa gtgcaacaat      960
tcaaagccca aaaagagtta cattgccaca caaggctgcc tgcaaaacac ggtgaatgac     1020
ttttggcgga tgggtgttcca agaaaactcc cgagtgattg tcatgacaac gaaagaagtg     1080
gagagaggaa agagtaaattg tgtcaaatac tggcctgatg agtatgctct aaaagaatat     1140

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[illegible]

ggcgtcatgc	gtgttaggaa	cgtcaaagaa	agcgccgctc	atgactatac	gctaagagaa	1200
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gacttcctgg	aggaggtgca	ccataagcag	gagagcatca	tggatgcagg	gccggctcgt	1380
gtgcactgca	gtgctggaat	tggccggaca	gggacgttca	ttgtgattga	tattcttatt	1440
gacatcatca	gagagaaagg	tgttgactgc	gatattgacg	ttcccaaaac	catccagatg	1500
gtgcgggtctc	agaggtcagg	gatggtccag	acagaagcac	agtaccgatt	tatctatatg	1560
gcgggtccagc	atttatattga	aacactacag	cgcaggattg	aagaagagca	gaaaagcaag	1620
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cagagccctc	tccgccttg	tactccaacg	ccaccctgtg	cagaaatgag	agaagacagt	1740
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<210> 22

<211> 597

<212> PRT

<213> Homo sapiens

<220>

<221> hSHP2_FL

<222> (1) . . (597)

<223>

<400> 22

Met	Thr	Ser	Arg	Arg	Trp	Phe	His	Pro	Asn	Ile	Thr	Gly	Val	Glu	Ala
1				5					10					15	

Glu Asn Leu Leu Leu Thr Arg Gly Val Asn Gly Ser Phe Leu Ala Arg
20 25 30

Pro Ser Lys Ser Asn Pro Gly Asp Phe Thr Leu Ser Val Arg Arg Asn
35 40 45

Gly Ala Val Thr His Ile Lys Ile Gln Asn Thr Gly Asp Tyr Tyr Asp
50 55 60

Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Ala Glu Leu Val Gln Tyr
65 70 75 80

Tyr Met Glu His His Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile
85 90 95

Glu Leu Lys Tyr Pro Leu Asn Cys Ala Asp Pro Thr Ser Glu Arg Trp
100 105 110

Phe His Gly His Leu Ser Gly Lys Glu Ala Glu Lys Leu Leu Thr Glu
115 120 125

Lys Gly Lys His Gly Ser Phe Leu Val Arg Glu Ser Gln Ser His Pro
130 135 140

Gly Asp Phe Val Leu Ser Val Arg Thr Gly Asp Asp Lys Gly Glu Ser
145 150 155 160

Asn Asp Gly Lys Ser Lys Val Thr His Val Met Ile Arg Cys Gln Glu
165 170 175

Leu Lys Tyr Asp Val Gly Gly Gly Glu Arg Phe Asp Ser Leu Thr Asp
180 185 190

Leu Val Glu His Tyr Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr
195 200 205

Val Leu Gln Leu Lys Gln Pro Leu Asn Thr Thr Arg Ile Asn Ala Ala
210 215 220

Glu Ile Glu Ser Arg Val Arg Glu Leu Ser Lys Leu Ala Glu Thr Thr
225 230 235 240

Asp Lys Val Lys Gln Gly Phe Trp Glu Glu Phe Glu Thr Leu Gln Gln
245 250 255

Gln Glu Cys Lys Leu Leu Tyr Ser Arg Lys Glu Gly Gln Arg Gln Glu
260 265 270

Asn Lys Asn Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Thr
275 280 285

Arg Val Val Leu His Asp Gly Asp Pro Asn Glu Pro Val Ser Asp Tyr
290 295 300

Ile Asn Ala Asn Ile Ile Met Pro Glu Phe Glu Thr Lys Cys Asn Asn
305 310 315 320

Ser Lys Pro Lys Lys Ser Tyr Ile Ala Thr Gln Gly Cys Leu Gln Asn
325 330 335

Thr Val Asn Asp Phe Trp Arg Met Val Phe Gln Glu Asn Ser Arg Val
340 345 350

Ile Val Met Thr Thr Lys Glu Val Glu Arg Gly Lys Ser Lys Cys Val
355 360 365

Lys Tyr Trp Pro Asp Glu Tyr Ala Leu Lys Glu Tyr Gly Val Met Arg
370 375 380

Val Arg Asn Val Lys Glu Ser Ala Ala His Asp Tyr Thr Leu Arg Glu
385 390 395 400

Leu Lys Leu Ser Lys Val Gly Gln Ala Leu Leu Gln Gly Asn Thr Glu
405 410 415

Arg Thr Val Trp Gln Tyr His Phe Arg Thr Trp Pro Asp His Gly Val
420 425 430

Pro Ser Asp Pro Gly Gly Val Leu Asp Phe Leu Glu Glu Val His His
435 440 445

Lys Gln Glu Ser Ile Met Asp Ala Gly Pro Val Val Val His Cys Ser
450 455 460

Ala Gly Ile Gly Arg Thr Gly Thr Phe Ile Val Ile Asp Ile Leu Ile
465 470 475 480

Asp Ile Ile Arg Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys
485 490 495

Thr Ile Gln Met Val Arg Ser Gln Arg Ser Gly Met Val Gln Thr Glu
500 505 510

Ala Gln Tyr Arg Phe Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr
515 520 525

Leu Gln Arg Arg Ile Glu Glu Glu Gln Lys Ser Lys Arg Lys Gly His
530 535 540

Glu Tyr Thr Asn Ile Lys Tyr Ser Leu Ala Asp Gln Thr Ser Gly Asp

545 550 555 560

Gln Ser Pro Leu Pro Pro Cys Thr Pro Thr Pro Pro Cys Ala Glu Met
 565 570 575

Arg Glu Asp Ser Ala Arg Val Tyr Glu Asn Val Gly Leu Met Gln Gln
 580 585 590

Gln Lys Ser Phe Arg
 595

<210> 23

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(396)

<223> Human OBRGRP

<400> 23

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cttatgctgg gatgtgcctt agaggattat ggcgtttact ggcccttatt cgtcctgatt 120

ttccacgcca tctcccccat ccccatcttc attgccaaaa ggtcaccta tgactcagat 180

gcaaccagta gtgcctgtcg ggaactggca tattttcttca ctactggaat tgttgtttct 240

gcctttggat ttctgttat tcttgctcgt gtggctgtga tcaaatgggg agcctgcggc 300

cttggtttgg caggcaatgc agtcattttc cttacaattc aagggttttt ccttatattt 360

ggaagaggag atgatttttag ctgggagcag tggtag 396

<210> 24

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> OBRGRP

<222> (1)..(131)

<223>

<400> 24

Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
1 5 10 15

Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
20 25 30

Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
35 40 45

His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
50 55 60

Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
65 70 75 80

Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
85 90 95

Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
100 105 110

Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
115 120 125

Glu Gln Trp
130

<210> 25

<211> 114

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(114)

<223> Human OBRGRP

<400> 25

attgccaaaa gagtcaccta tgactcagat gcaaccagta gtgcctgtcg ggaactggca 60

tatggatccc ttatatattgg aagaggagat gatttttagct gggagcagtg gtag 114

<210> 26

<211> 37

<212> PRT

<213> Homo sapiens

<220>

<221> OBRGRP

<222> (1)..(37)

<223>

<400> 26

Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser Ala Cys
1 5 10 15

Arg Glu Leu Ala Tyr Gly Ser Leu Ile Phe Gly Arg Gly Asp Asp Phe
20 25 30

Ser Trp Glu Gln Trp
35

<210> 27

<211> 87

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(87)

<223> Human Melatonin 1a receptor

<400> 27
 ggcacgcgcca tcaaccgcta ctgctacatc tgccacagtc tcaagtagca caaactgtac 60
 agcagcaaga actccctctg ctactag 87

<210> 28

<211> 28

<212> PRT

<213> Homo sapiens

<220>

<221> Melatonin 1a receptor

<222> (1)..(28)

<223>

<400> 28

Gly Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Lys Tyr
 1 5 10 15

Asp Lys Leu Tyr Ser Ser Lys Asn Ser Leu Cys Tyr
 20 25

<210> 29

<211> 90

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(90)

<223> Human Melatonin 1a receptor

<400> 29
 ctggttctcc aggtcagaca gagggtgaaa cctgaccgca aacccaaact gaaaccacag 60
 gacttcagga attttgtcac catgttttag 90

<210> 30

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> Melatonin 1a receptor

<222> (1)..(29)

<223>

<400> 30

Leu Val Leu Gln Val Arg Gln Arg Val Lys Pro Asp Arg Lys Pro Lys
 1 5 10 15

Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met Phe
 20 25

<210> 31

<211> 171

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(171)

<223> Human Melatonin 1a receptor

<400> 31
 tacgggctac tgaacaaaa ttccaggaag gaatacagga gaattatagt ctgcgtctgt 60

acagccaggg tgttctttgt ggacagctct aacgacgtgg ccgatagggt taaatggaaa 120
ccgtctccac tgatgaccaa caataatgta gtaaagggtg actccgttta a 171

<210> 32

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> Melatonin 1a receptor

<222> (1)..(56)

<223>

<400> 32

Tyr Gly Leu Leu Asn Gln Asn Phe Arg Lys Glu Tyr Arg Arg Ile Ile
1 5 10 15

Val Ser Leu Cys Thr Ala Arg Val Phe Phe Val Asp Ser Ser Asn Asp
20 25 30

Val Ala Asp Arg Val Lys Trp Lys Pro Ser Pro Leu Met Thr Asn Asn
35 40 45

Asn Val Val Lys Val Asp Ser Val
50 55

<210> 33

<211> 87

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(87)

<223> Human melatonin 1b receptor

<400> 33
gccatcgcca ttaaccgcta ctgctacatc tgccacagca tggcctacca ccgaatctac 60
cggcgctggc acacccctct gcactga 87

<210> 34
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> melatonin 1b receptor
<222> (1)..(28)
<223>

<400> 34
Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys His Ser Met Ala Tyr
1 5 10 15
His Arg Ile Tyr Arg Arg Trp His Thr Pro Leu His
20 25

<210> 35
<211> 90
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1)..(90)
<223> Human melatonin 1b receptor

<400> 35
ctggtgcttc aggcccgag gaaagccaag ccagagagca ggctgtgcct gaagcccagc 60

gacttgcgga gctttctaac catgttttga

90

<210> 36

<211> 29

<212> PRT

<213> Homo sapiens

<220>

<221> melatonin 1b receptor

<222> (1) .. (29)

<223>

<400> 36

Leu	Val	Leu	Gln	Ala	Arg	Arg	Lys	Ala	Lys	Pro	Glu	Ser	Arg	Leu	Cys
1				5					10					15	

Leu	Lys	Pro	Ser	Asp	Leu	Arg	Ser	Phe	Leu	Thr	Met	Phe
			20					25				

<210> 37

<211> 168

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (168)

<223> Human melatonin 1b receptor

<400> 37

tatgggctct	tgaacaaaa	cttccgcagg	gaatacaaga	ggatcctctt	ggccctttgg	60
aaccacggc	actgcattca	agatgcttcc	aagggcagcc	acgcggaggg	gctgcagagc	120
ccagctccac	ccatcattgg	tgtgcagcac	caggcagatg	ctctctag		168

<210> 38

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> melatonin 1b receptor

<222> (1)..(55)

<223>

<400> 38

Tyr Gly Leu Leu Asn Gln Asn Phe Arg Arg Glu Tyr Lys Arg Ile Leu
1 5 10 15

Leu Ala Leu Trp Asn Pro Arg His Cys Ile Gln Asp Ala Ser Lys Gly
20 25 30

Ser His Ala Glu Gly Leu Gln Ser Pro Ala Pro Pro Ile Ile Gly Val
35 40 45

Gln His Gln Ala Asp Ala Leu
50 55

<210> 39

<211> 120

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(120)

<223> Human OB-receptor short form

<400> 39

ggaacattat taatatcaca ccaaagaatg aaaaagctat tttgggaaga tggtccgaac 60

cccaagaatt gttcctgggc acaaggactt aattttcaga agagaacgga cattctttga 120

<210> 40

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> OB-receptor short form

<222> (1)..(39)

<223>

<400> 40

Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Glu
1				5					10					15	

Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly	Leu	Asn	Phe
			20					25					30		

Gln	Lys	Arg	Thr	Asp	Ile	Leu
						35

<210> 41

<211> 402

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(402)

<223> hOB-receptor long form

<400> 41
ggaacattat taatatcaca ccaaagaatg aaaaagctat tttgggaaga tggtccgaac 60

cccaagaatt gttcctgggc acaaggactt aattttcaga agccagaaac gtttgagcat 120
ctttttatca agcatacagc atcagtgaca tgtgggcctc ttcttttgga gcctgaaaca 180
atttcagaag atatcagtgt tgatacatca tggaaaaata aagatgagat gatgccaaca 240
actgtggtct ctctactttc aacaacagat cttgaaaagg gttctgtttg tattagtgac 300
cagttcaaca gtgttaactt ctctgaggct gaggggtactg aggtaaccta tgaggacgaa 360
agccagagac aaccctttgt taaatacgcc acgctgatct ag 402

<210> 42

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> hOB-receptor long form

<222> (1)..(133)

<223>

<400> 42

Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu Phe Trp Glu
1 5 10 15

Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly Leu Asn Phe
20 25 30

Gln Lys Pro Glu Thr Phe Glu His Leu Phe Ile Lys His Thr Ala Ser
35 40 45

Val Thr Cys Gly Pro Leu Leu Leu Glu Pro Glu Thr Ile Ser Glu Asp
50 55 60

Ile Ser Val Asp Thr Ser Trp Lys Asn Lys Asp Glu Met Met Pro Thr
65 70 75 80

Thr Val Val Ser Leu Leu Ser Thr Thr Asp Leu Glu Lys Gly Ser Val
85 90 95

Cys Ile Ser Asp Gln Phe Asn Ser Val Asn Phe Ser Glu Ala Glu Gly
100 105 110

Thr Glu Val Thr Tyr Glu Asp Glu Ser Gln Arg Gln Pro Phe Val Lys
 115 120 125

Tyr Ala Thr Leu Ile
 130

<210> 43

<211> 540

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(540)

<223> hOB-receptor long form

<400> 43
 gccacgctga tcagcaactc taaaccaagt gaaactggtg aagaacaagg gcttataaat 60
 agttcagtca ccaagtgctt ctctagcaaa aattctccat tgaaggattc tttctctaatt 120
 agctcatggg agatagaggc ccaggcattt tttatattat cagatcagca tcccaacata 180
 atttcaccac acctcacatt ctcagaagga ttggatgaac ttttgaaatt ggaggggaaat 240
 ttccctgaag aaaataatga taaaaagtct atctattatt taggggtcac ctcaatcaaa 300
 aagagagaga gtggtgtgct tttgactgac aagtcaaggg tatcgtgccc attcccagcc 360
 ccctgtttat tcacggacat cagagttctc caggacagtt gctcacactt tgtagaaaat 420
 aatatcaact taggaacttc tagtaagaag acttttgcac cttacatgcc tcaattccaa 480
 acttgttcta ctcagactca taagatcatg gaaaacaaga tgtgtgacct aactgtgtaa 540

<210> 44

<211> 179

<212> PRT

<213> Homo sapiens

<220>

<221> hOB-receptor long form

<222> (1)..(179)

<223>

<400> 44

Ala Thr Leu Ile Ser Asn Ser Lys Pro Ser Glu Thr Gly Glu Glu Gln
1 5 10 15

Gly Leu Ile Asn Ser Ser Val Thr Lys Cys Phe Ser Ser Lys Asn Ser
20 25 30

Pro Leu Lys Asp Ser Phe Ser Asn Ser Ser Trp Glu Ile Glu Ala Gln
35 40 45

Ala Phe Phe Ile Leu Ser Asp Gln His Pro Asn Ile Ile Ser Pro His
50 55 60

Leu Thr Phe Ser Glu Gly Leu Asp Glu Leu Leu Lys Leu Glu Gly Asn
65 70 75 80

Phe Pro Glu Glu Asn Asn Asp Lys Lys Ser Ile Tyr Tyr Leu Gly Val
85 90 95

Thr Ser Ile Lys Lys Arg Glu Ser Gly Val Leu Leu Thr Asp Lys Ser
100 105 110

Arg Val Ser Cys Pro Phe Pro Ala Pro Cys Leu Phe Thr Asp Ile Arg
115 120 125

Val Leu Gln Asp Ser Cys Ser His Phe Val Glu Asn Asn Ile Asn Leu
130 135 140

Gly Thr Ser Ser Lys Lys Thr Phe Ala Ser Tyr Met Pro Gln Phe Gln
145 150 155 160

Thr Cys Ser Thr Gln Thr His Lys Ile Met Glu Asn Lys Met Cys Asp
165 170 175

Leu Thr Val

<210> 45
 <211> 927
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (1)..(927)
 <223> hOB-receptor long form

<400> 45
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 cccaagaatt gttcctgggc acaaggactt aattttcaga agccagaaac gtttgagcat 120
 ctttttatca agcatacagc atcagtgcac tgtggtcctc ttcttttgga gcctgaaaca 180
 atttcagaag atatcagtgt tgatacatca tggaaaaata aagatgagat gatgccaaca 240
 actgtggtct ctctactttc aacaacagat cttgaaaagg gttctgtttg tattagtgcac 300
 cagttcaaca gtgttaactt ctctgaggct gaggggtactg aggtaacctg tgaggacgaa 360
 agccagagac aaccctttgt taaatacgcc acgctgatca gcaactctaa accaagtcaa 420
 actggtgaag aacaagggtt tataaatagt tcagtcacca agtgcttctc tagcaaaaat 480
 tctccattga aggattcttt ctctaatagc tcatgggaga tagaggccca ggcatttttt 540
 atattatcag atcagcatcc caacataatt tcaccacacc tcacattctc agaaggattg 600
 gatgaacttt tgaaattgga gggaaatttc cctgaagaaa ataatagataa aaagtctatc 660
 tattatttag gggtcacctc aatcaaaaag agagagagtg gtgtgctttt gactgacaag 720
 tcaagggtat cgtgcccatt cccagccccc tgtttattca cggacatcag agttctccag 780
 gacagttgct cacactttgt agaaaataat atcaacttag gaacttctag taagaagact 840
 tttgcattct acatgcctca attccaaact tgttctactc agactcataa gatcatggaa 900
 aacaagatgt gtgacctaac tgtgttaa 927

<210> 46
 <211> 308
 <212> PRT

<213> Homo sapiens

<220>

<221> hOB-receptor long form

<222> (1)..(308)

<223>

<400> 46

Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu Phe Trp Glu
1 5 10 15

Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly Leu Asn Phe
20 25 30

Gln Lys Pro Glu Thr Phe Glu His Leu Phe Ile Lys His Thr Ala Ser
35 40 45

Val Thr Cys Gly Pro Leu Leu Leu Glu Pro Glu Thr Ile Ser Glu Asp
50 55 60

Ile Ser Val Asp Thr Ser Trp Lys Asn Lys Asp Glu Met Met Pro Thr
65 70 75 80

Thr Val Val Ser Leu Leu Ser Thr Thr Asp Leu Glu Lys Gly Ser Val
85 90 95

Cys Ile Ser Asp Gln Phe Asn Ser Val Asn Phe Ser Glu Ala Glu Gly
100 105 110

Thr Glu Val Thr Tyr Glu Asp Glu Ser Gln Arg Gln Pro Phe Val Lys
115 120 125

Tyr Ala Thr Leu Ile Ser Asn Ser Lys Pro Ser Glu Thr Gly Glu Glu
130 135 140

Gln Gly Leu Ile Asn Ser Ser Val Thr Lys Cys Phe Ser Ser Lys Asn
145 150 155 160

Ser Pro Leu Lys Asp Ser Phe Ser Asn Ser Ser Trp Glu Ile Glu Ala
165 170 175

Gln Ala Phe Phe Ile Leu Ser Asp Gln His Pro Asn Ile Ile Ser Pro

180 185 190

His Leu Thr Phe Ser Glu Gly Leu Asp Glu Leu Leu Lys Leu Glu Gly
195 200 205

Asn Phe Pro Glu Glu Asn Asn Asp Lys Lys Ser Ile Tyr Tyr Leu Gly
210 215 220

Val Thr Ser Ile Lys Lys Arg Glu Ser Gly Val Leu Leu Thr Asp Lys
225 230 235 240

Ser Arg Val Ser Cys Pro Phe Pro Ala Pro Cys Leu Phe Thr Asp Ile
245 250 255

Arg Val Leu Gln Asp Ser Cys Ser His Phe Val Glu Asn Asn Ile Asn
260 265 270

Leu Gly Thr Ser Ser Lys Lys Thr Phe Ala Ser Tyr Met Pro Gln Phe
275 280 285

Gln Thr Cys Ser Thr Gln Thr His Lys Ile Met Glu Asn Lys Met Cys
290 295 300

Asp Leu Thr Val
305

<210> 47
<211> 2070
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1)..(2070)
<223> Human ADBR kinase 1

<400> 47
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aaggccacgc cggccgcgcg cgccagcaag aagatactgc tgcccgagcc cagcatccgc 120
agtgtcatgc agaagtacct ggaggaccgg ggcgaggtga cctttgagaa gatcttttcc 180

cagaagctgg ggtacctgct cttccgagac ttctgcctga accacctgga ggaggccagg 240
cccttggtgg aattctatga ggagatcaag aagtacgaga agctggagac ggaggaggag 300
cgtgtggccc gcagccggga gatcttcgac tcatacatca tgaaggagct gctggcctgc 360
tcgcataccct tctcgaagag tgccactgag catgtccaag gccacctggg gaagaagcag 420
gtgcctccgg atctcttcca gccatacatc gaagagattt gtcaaaacct ccgagggggac 480
gtgttccaga aattcattga gagcgataag ttcacacggt tttgccagtg gaagaatgtg 540
gagctcaaca tccacctgac catgaatgac ttcagcgtgc atcgcatcat tgggcgcggg 600
ggctttggcg aggtctatgg gtgccggaag gctgacacag gcaagatgta cgccatgaag 660
tgcttggaaca aaaagcgcac caagatgaag cagggggaga ccctggccct gaacgagcgc 720
atcatgctct cgctcgtcag cactggggac tgccattca ttgtctgcat gtcatacgcg 780
ttccacacgc cagacaagct cagcttcac ctaggacctca tgaacggtgg ggacctgcac 840
taccacctct ccagcacagg ggtcttctca gaggctgaca tgcgcttcta tgcggccgag 900
atcatcctgg gcctggagca catgcacaac cgcttcgtgg tctaccggga cctgaagcca 960
gccaacatcc ttctggacga gcatggccac gtgcggatct cggacctggg cctggcctgt 1020
gacttctcca agaagaagcc ccatgccagc gtgggcaccc acgggtacat ggctccggag 1080
gtcctgcaga agggcgtggc ctacgacagc agtgccgact gggtctctct ggggtgcatg 1140
ctcttcaagt tgctgcgggg gcacagcccc ttccggcagc acaagaccaa agacaagcat 1200
gagatcgacc gcatgacgct gacgatggcc gtggagctgc ccgactcctt ctcccctgaa 1260
ctacgctccc tgctggaggg gttgctgcag agggatgtca accggagatt gggctgcctg 1320
ggccgagggg ctcaggaggt gaaagagagc ccctttttcc gctccctgga ctggcagatg 1380
gtcttcttgc agaagtaccc tcccccgctg atccccccac gaggggaggt gaacgcggcc 1440
gacgccttcg acattggctc cttcgatgag gaggacacaa aaggaatcaa gttactggac 1500
agtgatcagg agctctaccg caacttcccc ctcacatct cggagcggtg gcagcaggag 1560
gtggcagaga ctgtcttcga caccatcaac gctgagacag accggctgga ggctcgcaag 1620
aaagccaaga acaagcagct gggccatgag gaagactacg ccctgggcaa ggactgcatc 1680
atgcatggct acatgtccaa gatgggcaac cccttctga ccagtgga gcggcggtac 1740
ttctacctgt tccccaccg cctcgagtgg cggggcgagg gcgaggcccc gcagagcctg 1800
ctgaccatgg aggagatcca gtcggtggag gagacgcaga tcaaggagcg caagtgcctg 1860
ctcctcaaga tccgcggtgg gaaacagttc attttgagc gcgatagcga ccctgagctg 1920
gtgcagtgga agaaggagct gcgcgacgcc taccgcgagg ccagcagct ggtgcagcgg 1980

gtgcccaaga tgaagaacaa gccgcgctcg cccgtggtgg agctgagcaa ggtgccgctg 2040
gtccagcgcg gcagtgccaa cggcctctga 2070

<210>	48
<211>	689
<212>	PRT
<213>	Homo sapiens

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<220>
<221>  ADBR kinase 1
<222>  (1)..(689)
<223>
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<400> 48

Met Ala Asp Leu Glu Ala Val Leu Ala Asp Val Ser Tyr Leu Met Ala
1 5 10 15

Met Glu Lys Ser Lys Ala Thr Pro Ala Ala Arg Ala Ser Lys Lys Ile
20 25 30

Leu Leu Pro Glu Pro Ser Ile Arg Ser Val Met Gln Lys Tyr Leu Glu
35 40 45

Asp Arg Gly Glu Val Thr Phe Glu Lys Ile Phe Ser Gln Lys Leu Gly
50 55 60

Tyr Leu Leu Phe Arg Asp Phe Cys Leu Asn His Leu Glu Glu Ala Arg
65 70 75 80

Pro Leu Val Glu Phe Tyr Glu Glu Ile Lys Lys Tyr Glu Lys Leu Glu
85 90 95

Thr Glu Glu Glu Arg Val Ala Arg Ser Arg Glu Ile Phe Asp Ser Tyr
100 105 110

Ile Met Lys Glu Leu Leu Ala Cys Ser His Pro Phe Ser Lys Ser Ala
115 120 125

Thr Glu His Val Gln Gly His Leu Gly Lys Lys Gln Val Pro Pro Asp
130 135 140

$$\begin{aligned} \frac{1}{\sqrt{1-\beta^2}} &= \frac{1}{\sqrt{1-\frac{v^2}{c^2}}} = \frac{1}{\sqrt{1-\frac{1}{9}}} = \frac{1}{\sqrt{\frac{8}{9}}} = \frac{3}{2\sqrt{2}} = \frac{3\sqrt{2}}{4} \approx 1.06066 \\ \gamma &= \frac{1}{\sqrt{1-\beta^2}} = \frac{3\sqrt{2}}{4} \approx 1.06066 \\ \gamma v &= \frac{3\sqrt{2}}{4} \cdot \frac{c}{3} = \frac{\sqrt{2}}{4} c \approx 0.35355 c \\ \gamma \frac{v}{c} &= \frac{\sqrt{2}}{4} \approx 0.35355 \\ \gamma \frac{v^2}{c^2} &= \frac{\sqrt{2}}{4} \cdot \frac{1}{3} = \frac{\sqrt{2}}{12} \approx 0.11785 \\ \gamma \frac{v^3}{c^3} &= \frac{\sqrt{2}}{12} \cdot \frac{1}{3} = \frac{\sqrt{2}}{36} \approx 0.03928 \\ \gamma \frac{v^4}{c^4} &= \frac{\sqrt{2}}{36} \cdot \frac{1}{3} = \frac{\sqrt{2}}{108} \approx 0.01309 \\ \gamma \frac{v^5}{c^5} &= \frac{\sqrt{2}}{108} \cdot \frac{1}{3} = \frac{\sqrt{2}}{324} \approx 0.00436 \\ \gamma \frac{v^6}{c^6} &= \frac{\sqrt{2}}{324} \cdot \frac{1}{3} = \frac{\sqrt{2}}{972} \approx 0.00145 \\ \gamma \frac{v^7}{c^7} &= \frac{\sqrt{2}}{972} \cdot \frac{1}{3} = \frac{\sqrt{2}}{2916} \approx 0.00048 \\ \gamma \frac{v^8}{c^8} &= \frac{\sqrt{2}}{2916} \cdot \frac{1}{3} = \frac{\sqrt{2}}{8748} \approx 0.00016 \\ \gamma \frac{v^9}{c^9} &= \frac{\sqrt{2}}{8748} \cdot \frac{1}{3} = \frac{\sqrt{2}}{26244} \approx 5.2 \times 10^{-5} \\ \gamma \frac{v^{10}}{c^{10}} &= \frac{\sqrt{2}}{26244} \cdot \frac{1}{3} = \frac{\sqrt{2}}{78732} \approx 1.7 \times 10^{-5} \end{aligned}$$

Val Phe Gln Lys Phe Ile Glu Ser Asp Lys Phe Thr Arg Phe Cys Gln
165 170 175

Trp Lys Asn Val Glu Leu Asn Ile His Leu Thr Met Asn Asp Phe Ser
180 185 190

Val His Arg Ile Ile Gly Arg Gly Gly Phe Gly Glu Val Tyr Gly Cys
195 200 205

Arg Lys Ala Asp Thr Gly Lys Met Tyr Ala Met Lys Cys Leu Asp Lys
210 215 220

Lys Arg Ile Lys Met Lys Gln Gly Glu Thr Leu Ala Leu Asn Glu Arg
225 230 235 240

Ile Met Leu Ser Leu Val Ser Thr Gly Asp Cys Pro Phe Ile Val Cys
245 250 255

Met Ser Tyr Ala Phe His Thr Pro Asp Lys Leu Ser Phe Ile Leu Asp
260 265 270

Leu Met Asn Gly Gly Asp Leu His Tyr His Leu Ser Gln His Gly Val
275 280 285

Phe Ser Glu Ala Asp Met Arg Phe Tyr Ala Ala Glu Ile Ile Leu Gly
290 295 300

```
Leu Glu His Met His Asn Arg Phe Val Val Tyr Arg Asp Leu Lys Pro  
305                      310                315          320
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Ala Asn Ile Leu Leu Asp Glu His Gly His Val Arg Ile Ser Asp Leu
325 330 335

Gly Leu Ala Cys Asp Phe Ser Lys Lys Lys Pro His Ala Ser Val Gly
340 345 350

Thr His Gly Tyr Met Ala Pro Glu Val Leu Gln Lys Gly Val Ala Tyr
355 360 365

Asp Ser Ser Ala Asp Trp Phe Ser Leu Gly Cys Met Leu Phe Lys Leu
370 375 380

Leu Arg Gly His Ser Pro Phe Arg Gln His Lys Thr Lys Asp Lys His
385 390 395 400

Glu Ile Asp Arg Met Thr Leu Thr Met Ala Val Glu Leu Pro Asp Ser
405 410 415

Phe Ser Pro Glu Leu Arg Ser Leu Leu Glu Gly Leu Leu Gln Arg Asp
420 425 430

Val Asn Arg Arg Leu Gly Cys Leu Gly Arg Gly Ala Gln Glu Val Lys
435 440 445

Glu Ser Pro Phe Phe Arg Ser Leu Asp Trp Gln Met Val Phe Leu Gln
450 455 460

Lys Tyr Pro Pro Pro Leu Ile Pro Pro Arg Gly Glu Val Asn Ala Ala
465 470 475 480

Asp Ala Phe Asp Ile Gly Ser Phe Asp Glu Glu Asp Thr Lys Gly Ile
485 490 495

Lys Leu Leu Asp Ser Asp Gln Glu Leu Tyr Arg Asn Phe Pro Leu Thr
500 505 510

Ile Ser Glu Arg Trp Gln Gln Glu Val Ala Glu Thr Val Phe Asp Thr
515 520 525

Ile Asn Ala Glu Thr Asp Arg Leu Glu Ala Arg Lys Lys Ala Lys Asn
530 535 540

Lys Gln Leu Gly His Glu Glu Asp Tyr Ala Leu Gly Lys Asp Cys Ile
545 550 555 560

Met His Gly Tyr Met Ser Lys Met Gly Asn Pro Phe Leu Thr Gln Trp
565 570 575

Gln Arg Arg Tyr Phe Tyr Leu Phe Pro Asn Arg Leu Glu Trp Arg Gly
580 585 590

Glu Gly Glu Ala Pro Gln Ser Leu Leu Thr Met Glu Glu Ile Gln Ser
595 600 605

Val Glu Glu Thr Gln Ile Lys Glu Arg Lys Cys Leu Leu Leu Lys Ile
610 615 620

Arg Gly Gly Lys Gln Phe Ile Leu Gln Cys Asp Ser Asp Pro Glu Leu
 625 630 635 640

Val Gln Trp Lys Lys Glu Leu Arg Asp Ala Tyr Arg Glu Ala Gln Gln
 645 650 655

Leu Val Gln Arg Val Pro Lys Met Lys Asn Lys Pro Arg Ser Pro Val
 660 665 670

Val Glu Leu Ser Lys Val Pro Leu Val Gln Arg Gly Ser Ala Asn Gly
 675 680 685

Leu

<210> 49

<211> 2067

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2067)

<223> Rat ADBR kinase 2

<400> 49

atggcgagacc tggaggccgt gctggccgat gtcagttacc tgatggccat ggagaagagc	60
aaggcgaccc cggccgcccg cgccagcaag aggatcgctc tgccggagcc cagtatccgg	120
agtgatgatgc agaagtacct tgcagagaga aatgaaataa cctttgacaa gattttcaat	180
cagaaaattg gtttcttgct atttaaagat ttttgtttga atgaaattaa tgaagctgta	240
cctcaggtga agttttatga agagataaag gaatatgaaa aacttgataa tgaggaagac	300
cgcttttgca gaagtcgaca aatttatgat gcctacatca tgaaggaact tctttcctgt	360
tcacatcctt tctcaaagca agctgtagaa cacgtacaaa gtcatttatc caagaaacaa	420
gtgacatcaa ctcttttttca gccatacata gaagaaatth gtgaaagcct tcgaggtgac	480
atcttttcaa aatttatgga aagtgacaag ttcactagat tttgtcagtg gaaaaacgtt	540
gaattaaata tccatttgac catgaatgag ttcagtgtgc ataggattat tggacgagga	600

ggattcgggg aagtttatgg ttgcaggaaa gcagacactg gaaaaatgta tgcaatgaaa 660
tgcttagata agaagaggat caaaatgaaa caaggagaaa cattagcctt aaatgaaaga 720
atcatgttgt ctcttgtcag cacaggagac tgtcctttca ttgtatgtat gacctatgcc 780
ttccataccc cagataaaact ctgcttcac caggatctga tgaacggggg cgatttgcac 840
taccaccttt cacaacacgg tgtgttctct gagaaggaga tgcggtttta tgccactgaa 900
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gcaaatatc tcttgatga acatggacac gcaagaatat cagatcttgg tcttgctgc 1020
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gatgcctttg atattggctc atttgatgaa gaggatacca aagggattaa gctacttgat 1500
tgcgaccaag aactctacaa gaacttcct ttggtcatct ctgaacgctg gcagcaagaa 1560
gtaacggaaa cagtttatga agcagtaa atgcagacag ataaaatcga ggccaggaag 1620
agagctaaaa ataagcaact tggccacgaa gaagattacg ctctggggaa ggactgtatt 1680
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ttttacctct ttccaaatag acttgaatgg agaggagagg gagagtcccg gcaaaattta 1800
ctgacaatgg aacagattct ctctgtggaa gaaactcaaa ttaaagacaa aaaatgcatt 1860
ttgttcagaa taaaaggagg gaaacaatgt gtcttgcaat gtgagagtga tccagagttt 1920
gtgcagtgga agaaagagtt gaacgaaacc ttcaaggagg cccagcggct attgcgtcgt 1980
gccccgaagt tcctcaacaa acctcggtca ggtactgtgg agctcccaa gccatccctc 2040
tgtcacagaa atagcagcgg cctctga 2067

<210> 50

<211> 688

<212> PRT

<213> Homo sapiens

<220>

<221> ADBR kinase 2

<222> (1)..(688)

<223>

<400> 50

Met Ala Asp Leu Glu Ala Val Leu Ala Asp Val Ser Tyr Leu Met Ala
1 5 10 15

Met Glu Lys Ser Lys Ala Thr Pro Ala Ala Arg Ala Ser Lys Arg Ile
20 25 30

Val Leu Pro Glu Pro Ser Ile Arg Ser Val Met Gln Lys Tyr Leu Ala
35 40 45

Glu Arg Asn Glu Ile Thr Phe Asp Lys Ile Phe Asn Gln Lys Ile Gly
50 55 60

Phe Leu Leu Phe Lys Asp Phe Cys Leu Asn Glu Ile Asn Glu Ala Val
65 70 75 80

Pro Gln Val Lys Phe Tyr Glu Glu Ile Lys Glu Tyr Glu Lys Leu Asp
85 90 95

Asn Glu Glu Asp Arg Leu Cys Arg Ser Arg Gln Ile Tyr Asp Ala Tyr
100 105 110

Ile Met Lys Glu Leu Leu Ser Cys Ser His Pro Phe Ser Lys Gln Ala
115 120 125

Val Glu His Val Gln Ser His Leu Ser Lys Lys Gln Val Thr Ser Thr
130 135 140

Leu Phe Gln Pro Tyr Ile Glu Glu Ile Cys Glu Ser Leu Arg Gly Asp
145 150 155 160

Ile Phe Gln Lys Phe Met Glu Ser Asp Lys Phe Thr Arg Phe Cys Gln
165 170 175

Trp Lys Asn Val Glu Leu Asn Ile His Leu Thr Met Asn Glu Phe Ser
180 185 190

Val His Arg Ile Ile Gly Arg Gly Gly Phe Gly Glu Val Tyr Gly Cys

195		200		205
Arg Lys Ala Asp Thr Gly Lys Met Tyr Ala Met Lys Cys Leu Asp Lys				
210		215		220
Lys Arg Ile Lys Met Lys Gln Gly Glu Thr Leu Ala Leu Asn Glu Arg				
225		230		235 240
Ile Met Leu Ser Leu Val Ser Thr Gly Asp Cys Pro Phe Ile Val Cys				
	245		250	255
Met Thr Tyr Ala Phe His Thr Pro Asp Lys Leu Cys Phe Ile Leu Asp				
	260		265	270
Leu Met Asn Gly Gly Asp Leu His Tyr His Leu Ser Gln His Gly Val				
	275		280	285
Phe Ser Glu Lys Glu Met Arg Phe Tyr Ala Thr Glu Ile Ile Leu Gly				
	290		295	300
Leu Glu His Met His Asn Arg Phe Val Val Tyr Arg Asp Leu Lys Pro				
305		310		315 320
Ala Asn Ile Leu Leu Asp Glu His Gly His Ala Arg Ile Ser Asp Leu				
	325		330	335
Gly Leu Ala Cys Asp Phe Ser Lys Lys Lys Pro His Ala Ser Val Gly				
	340		345	350
Thr His Gly Tyr Met Ala Pro Glu Val Leu Gln Lys Gly Thr Ala Tyr				
	355		360	365
Asp Ser Ser Ala Asp Trp Phe Ser Leu Gly Cys Met Leu Phe Lys Leu				
	370		375	380
Leu Arg Gly His Ser Pro Phe Arg Gln His Lys Thr Lys Asp Lys His				
385		390		395 400
Glu Ile Asp Arg Met Thr Leu Thr Val Asn Val Glu Leu Pro Asp Thr				
	405		410	415
Phe Ser Pro Glu Leu Lys Ser Leu Leu Glu Gly Leu Leu Gln Arg Asp				
	420		425	430
Val Ser Lys Arg Leu Gly Cys His Gly Gly Gly Ser Gln Glu Val Lys				
	435		440	445

Glu His Ser Phe Phe Lys Gly Val Asp Trp Gln His Val Tyr Leu Gln
450 455 460

Lys Tyr Pro Pro Pro Leu Ile Pro Pro Arg Gly Glu Val Asn Ala Ala
465 470 475 480

Asp Ala Phe Asp Ile Gly Ser Phe Asp Glu Glu Asp Thr Lys Gly Ile
485 490 495

Lys Leu Leu Asp Cys Asp Gln Glu Leu Tyr Lys Asn Phe Pro Leu Val
500 505 510

Ile Ser Glu Arg Trp Gln Gln Glu Val Thr Glu Thr Val Tyr Glu Ala
515 520 525

Val Asn Ala Asp Thr Asp Lys Ile Glu Ala Arg Lys Arg Ala Lys Asn
530 535 540

Lys Gln Leu Gly His Glu Glu Asp Tyr Ala Leu Gly Lys Asp Cys Ile
545 550 555 560

Met His Gly Tyr Met Leu Lys Leu Gly Asn Pro Phe Leu Thr Gln Trp
565 570 575

Gln Arg Arg Tyr Phe Tyr Leu Phe Pro Asn Arg Leu Glu Trp Arg Gly
580 585 590

Glu Gly Glu Ser Arg Gln Asn Leu Leu Thr Met Glu Gln Ile Leu Ser
595 600 605

Val Glu Glu Thr Gln Ile Lys Asp Lys Lys Cys Ile Leu Phe Arg Ile
610 615 620

Lys Gly Gly Lys Gln Phe Val Leu Gln Cys Glu Ser Asp Pro Glu Phe
625 630 635 640

Val Gln Trp Lys Lys Glu Leu Asn Glu Thr Phe Lys Glu Ala Gln Arg
645 650 655

Leu Leu Arg Arg Ala Pro Lys Phe Leu Asn Lys Pro Arg Ser Gly Thr
660 665 670

Val Glu Leu Pro Lys Pro Ser Leu Cys His Arg Asn Ser Ser Gly Leu
675 680 685

<210> 51
 <211> 1359
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> gene
 <222> (1) .. (1359)
 <223> Rat beta Arrestin 1

<400> 51
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 tatctgggaa agcgggactt tgtggaccac atcgacctcg tggagcccggt ggatggagtg 120
 gttcttctgtg atccggagta tctcaaggag aggagagtct atgtgacgct gacctgcgcc 180
 ttccgctacg gccgggagga cctggatgtc ctgggcctga cctttcgcaa ggacctgttt 240
 gtggccaacg tgcagtcttt cccgccggcc cctgaggaca agaagcccct gacgcggctg 300
 caggagcgcc tcatcaagaa gctgggagag catgcctacc ctttcacctt tgagatccct 360
 ccgaacctcc catgctctgt gactttgcag ccgggacctg aagatacagg gaaggcctgc 420
 ggtgtggact acgaagtga agccttctgt gcggagaacc tggaggagaa gatccacaag 480
 cggaattctg tgcgcctggt catccggaag gttcagtatg cccagagag gcttggcccc 540
 cagcccacgg ccgagaccac caggcagttc ctcatgtcag acaagccctt gcatctggag 600
 gcctccctgg acaaggagat ctactaccac ggagaaccca tcagtgtcaa cgtccatgtc 660
 accaacaaca ccaacaagac ggtgaagaag atcaagatct cgggtgcgcca gtatgcagac 720
 atctgtctgt tcaacacagc ccagtacaag tgccctgtgg ccatggaaga ggctgatgac 780
 acagtggcac ccagctctac gttctgcaag gtctacacgc tgacccccctt cctggccaac 840
 aatcgagaga agcggggcct cgccctggac gggaagctca aacacgagga cacgaacctg 900
 gcctccagca ccctgttgag ggaaggagcc aaccgggaga tcctgggcat cattgtttcc 960
 tacaaagtga aagtgaagct ggtggtgtct cgtggcggcc tgttgggaga tcttgcattc 1020
 agtgatgtgg ccgtggaact gcctttcacc ctaatgcacc ccaagcccaa agaggaaccc 1080
 ccacaccggg aagttccaga gcacgagacg ccggtagata ccaatctcat agaacttgac 1140
 accaacgatg acgacattgt gtttgaggac tttgcccgcc agagactaaa aggcattgaag 1200

gatgacaagg aggaagagga ggatggtacc ggctctccgc ggacgcgtga gctcagatct 1260
 cccatgtctc tactggtggt ggtgcttctt tggaattatt ggaaggtaag gaattgccag 1320
 gtgttgcttt cttatccgaa aagaaataaa ttgaattga 1359

<210> 52

<211> 452

<212> PRT

<213> Homo sapiens

<220>

<221> beta Arrestin 1

<222> (1)..(452)

<223>

<400> 52

Met Gly Asp Lys Gly Thr Arg Val Phe Lys Lys Ala Ser Pro Asn Gly
 1 5 10 15

Lys Leu Thr Val Tyr Leu Gly Lys Arg Asp Phe Val Asp His Ile Asp
 20 25 30

Leu Val Glu Pro Val Asp Gly Val Val Leu Val Asp Pro Glu Tyr Leu
 35 40 45

Lys Glu Arg Arg Val Tyr Val Thr Leu Thr Cys Ala Phe Arg Tyr Gly
 50 55 60

Arg Glu Asp Leu Asp Val Leu Gly Leu Thr Phe Arg Lys Asp Leu Phe
 65 70 75 80

Val Ala Asn Val Gln Ser Phe Pro Pro Ala Pro Glu Asp Lys Lys Pro
 85 90 95

Leu Thr Arg Leu Gln Glu Arg Leu Ile Lys Lys Leu Gly Glu His Ala
 100 105 110

Tyr Pro Phe Thr Phe Glu Ile Pro Pro Asn Leu Pro Cys Ser Val Thr
 115 120 125

[illegible]

Leu Gln Pro Gly Pro Glu Asp Thr Gly Lys Ala Cys Gly Val Asp Tyr
130 135 140

Glu Val Lys Ala Phe Cys Ala Glu Asn Leu Glu Glu Lys Ile His Lys
145 150 155 160

Arg	Asn	Ser	Val	Arg	Leu	Val	Ile	Arg	Lys	Val	Gln	Tyr	Ala	Pro	Glu
				165					170					175	

Arg Pro Gly Pro Gln Pro Thr Ala Glu Thr Thr Arg Gln Phe Leu Met
180 185 190

Ser Asp Lys Pro Leu His Leu Glu Ala Ser Leu Asp Lys Glu Ile Tyr
195 200 205

Tyr	His	Gly	Glu	Pro	Ile	Ser	Val	Asn	Val	His	Val	Thr	Asn	Asn	Thr
210						215					220				

Asn Lys Thr Val Lys Lys Ile Lys Ile Ser Val Arg Gln Tyr Ala Asp
225 230 235 240

Ile Cys Leu Phe Asn Thr Ala Gln Tyr Lys Cys Pro Val Ala Met Glu
245 250 255

Glu Ala Asp Asp Thr Val Ala Pro Ser Ser Thr Phe Cys Lys Val Tyr
260 265 270

Thr Leu Thr Pro Phe Leu Ala Asn Asn Arg Glu Lys Arg Gly Leu Ala
275 280 285

Leu Asp Gly Lys Leu Lys His Glu Asp Thr Asn Leu Ala Ser Ser Thr
290 295 300

Leu Leu Arg Glu Gly Ala Asn Arg Glu Ile Leu Gly Ile Ile Val Ser
305 310 315 320

Tyr Lys Val Lys Val Lys Leu Val Val Ser Arg Gly Gly Leu Leu Gly
325 330 335

Asp Leu Ala Ser Ser Asp Val Ala Val Glu Leu Pro Phe Thr Leu Met
340 345 350

His Pro Lys Pro Lys Glu Glu Pro Pro His Arg Glu Val Pro Glu His
355 360 365

Glu Thr Pro Val Asp Thr Asn Leu Ile Glu Leu Asp Thr Asn Asp Asp
370 375 380

Asp Ile Val Phe Glu Asp Phe Ala Arg Gln Arg Leu Lys Gly Met Lys
385 390 395 400

Asp Asp Lys Glu Glu Glu Glu Asp Gly Thr Gly Ser Pro Arg Thr Arg
405 410 415

Glu Leu Arg Ser Pro Met Ser Leu Leu Val Val Val Leu Leu Trp Asn
420 425 430

Tyr Trp Lys Val Arg Asn Cys Gln Val Leu Leu Ser Tyr Pro Lys Arg
435 440 445

Asn Lys Leu Asn
450

<210> 53

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1) .. (1233)

<223> Rat beta Arrestin2

<400> 53
atgggtgaaa aaccgggac cagggctctc aagaagtcga gccctaactg caagctcacc 60
gtgtacttgg gcaagcgtga ctttgtggat cacttggaaca aagtggatcc tgtcgatggg 120
gtgggtgcttg tggatcctga ctacttgaag gaccggaaaag tgtttgtgac cctcacctgt 180
gccttccgct atggccgaga agacctggat gtactggggcc tgtctttccg caaagatctg 240
ttcatcgcca cctaccaggc cttccccccc atgcccaacc cacctcgggc cccacccgc 300
ctacaggacc gactgctgaa gaagttgggc cagcatgccc accccttttt tttcacaata 360
ccccagaatt tgccttgctc cgtcacactg cagccaggac cggaggacac aggggaaggcc 420
tgtggagtag actttgagat tcgagccttc tgtgccaat ctatagaaga aaaaagccac 480

aaaaggaact ccgtgcggct tatcatcaga aaggtacagt ttgctcctga gacacccggc 540
 cccagccat cagctgaaac cacacgccac ttctcatgt ctgaccggag gtccctgcac 600
 ctagaggett ccctggacaa agagctgtac taccatgggg aaccctcaa tgtcaacgtc 660
 cacgtcacca acaattctgc caagaccgtc aagaagatca gagtgtctgt gagacagtat 720
 gccgacattt gcctcttcag caccgcgcag tacaagtgtc ctgtggctca gcttgaacaa 780
 gatgaccagg tgttctccag ttccacattc tgcaagggtg acaccataac cccgctgctc 840
 agtgacaacc gagagaagcg tggccttgcc cttgatgggc aactcaagca cgaagacacc 900
 aacctggctt ccagcaccat tgtgaaggag ggagccaaca aggaggtgct ggggaatccta 960
 gtatcctaca gggtaagggt gaagctgggt gtgtctcgag gcggggatgt ctccgtggag 1020
 ctacctttcg tcctaataga cccaagccc caccaccaca tcaccttcc ccgaccccag 1080
 tcagcccccc gggaaataga catccctgtg gataccaacc tcattgaatt cgataccaac 1140
 tatgccacag acgacgacat cgtgtttgag gactttgcga ggcttcggct gaaggggatg 1200
 aaggatgacg actgtgatga ccagttctgc tag 1233

<210> 54

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<221> beta Arrestin2

<222> (1)..(410)

<223>

<400> 54

Met Gly Glu Lys Pro Gly Thr Arg Val Phe Lys Lys Ser Ser Pro Asn
 1 5 10 15

Cys Lys Leu Thr Val Tyr Leu Gly Lys Arg Asp Phe Val Asp His Leu
 20 25 30

Asp Lys Val Asp Pro Val Asp Gly Val Val Leu Val Asp Pro Asp Tyr
 35 40 45

Leu Lys Asp Arg Lys Val Phe Val Thr Leu Thr Cys Ala Phe Arg Tyr
50 55 60

Gly Arg Glu Asp Leu Asp Val Leu Gly Leu Ser Phe Arg Lys Asp Leu
65 70 75 80

Phe Ile Ala Thr Tyr Gln Ala Phe Pro Pro Met Pro Asn Pro Pro Arg
85 90 95

Pro Pro Thr Arg Leu Gln Asp Arg Leu Leu Lys Lys Leu Gly Gln His
100 105 110

Ala His Pro Phe Phe Phe Thr Ile Pro Gln Asn Leu Pro Cys Ser Val
115 120 125

Thr Leu Gln Pro Gly Pro Glu Asp Thr Gly Lys Ala Cys Gly Val Asp
130 135 140

Phe Glu Ile Arg Ala Phe Cys Ala Lys Ser Ile Glu Glu Lys Ser His
145 150 155 160

Lys Arg Asn Ser Val Arg Leu Ile Ile Arg Lys Val Gln Phe Ala Pro
165 170 175

Glu Thr Pro Gly Pro Gln Pro Ser Ala Glu Thr Thr Arg His Phe Leu
180 185 190

Met Ser Asp Arg Arg Ser Leu His Leu Glu Ala Ser Leu Asp Lys Glu
195 200 205

Leu Tyr Tyr His Gly Glu Pro Leu Asn Val Asn Val His Val Thr Asn
210 215 220

Asn Ser Ala Lys Thr Val Lys Lys Ile Arg Val Ser Val Arg Gln Tyr
225 230 235 240

Ala Asp Ile Cys Leu Phe Ser Thr Ala Gln Tyr Lys Cys Pro Val Ala
245 250 255

Gln Leu Glu Gln Asp Asp Gln Val Ser Pro Ser Ser Thr Phe Cys Lys
260 265 270

Val Tyr Thr Ile Thr Pro Leu Leu Ser Asp Asn Arg Glu Lys Arg Gly
275 280 285

Leu Ala Leu Asp Gly Gln Leu Lys His Glu Asp Thr Asn Leu Ala Ser

290 295 300

Ser Thr Ile Val Lys Glu Gly Ala Asn Lys Glu Val Leu Gly Ile Leu
305 310 315 320

Val Ser Tyr Arg Val Lys Val Lys Leu Val Val Ser Arg Gly Gly Asp
325 330 335

Val Ser Val Glu Leu Pro Phe Val Leu Met His Pro Lys Pro His Asp
340 345 350

His Ile Thr Leu Pro Arg Pro Gln Ser Ala Pro Arg Glu Ile Asp Ile
355 360 365

Pro Val Asp Thr Asn Leu Ile Glu Phe Asp Thr Asn Tyr Ala Thr Asp
370 375 380

Asp Asp Ile Val Phe Glu Asp Phe Ala Arg Leu Arg Leu Lys Gly Met
385 390 395 400

Lys Asp Asp Asp Cys Asp Asp Gln Phe Cys
405 410

<210> 55

<211> 2313

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2313)

<223> human STAT3 : Transcription factor; Phosphorylation by JAK-type k
inases leads to dimersiation and translocation to the nucleus to
transactivate target gene expression

<400> 55

atggcccaat ggaatcagct acagcagctt gacacacggt acctggagca gctccatcag 60

ctctacagtg acagcttccc aatggagctg cggcagtttc tggcccttg gattgagagt 120

caagattggg catatgcggc cagcaaagaa tcacatgcca ctttggtgtt tcataatctc 180

ctgggagaga ttgaccagca gtatagccgc ttctgcaag agtcgaatgt tctctatcag 240

cacaatctac gaagaatcaa gcagtttctt cagagcaggt atctggagaa gccaatggag 300
 attgcccgga ttgtggcccg gtgcctgtgg gaagaatcac gccttctaca gactgcagcc 360
 actgcggccc agcaaggggg ccaggccaac caccacacag cagccgtggt gacggagaag 420
 cagcagatgc tggagcagca ccttcaggat gtccggaaga gagtgcagga tctagaacag 480
 aaaatgaaag tggtagagaa tctccaggat gactttgatt tcaactataa aaccctcaag 540
 agtcaaggag acatgcaaga tctgaatgga aacaaccagt cagtgaccag gcagaagatg 600
 cagcagctgg aacagatgct cactgcgctg gaccagatgc ggagaagcat cgtgagttag 660
 ctggcggggc ttttgtcagc gatggagtac gtgcagaaaa ctctcacgga cgaggagctg 720
 gctgactgga agaggcggca acagattgcc tgcattggag gcccgcccaa catctgccta 780
 gatcggctag aaaactggat aacgtcatta gcagaatctc aacttcagac ccgtcaacaa 840
 attaagaaac tggaggagtt gcagcaaaaa gtttcctaca aaggggaccc cattgtacag 900
 caccggccga tgctggagga gagaatcgtg gagctgttta gaaacttaat gaaaagtgcc 960
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 accggcgtcc agttcactac taaagtcagg ttgctggtca aattccctga gttgaattat 1080
 cagcttaaaa ttaaagtgtg cattgacaaa gactctgggg acgttgacgc tctcagagga 1140
 tcccggaaat ttaacattct gggcacaaac acaaaagtga tgaacatgga agaatccaac 1200
 aacggcagcc tctctgcaga attcaaacac ttgaccctga gggagcagag atgtgggaat 1260
 gggggccgag ccaattgtga tgcttccttg attgtgactg aggagctgca cctgatcacc 1320
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 tgggatcaag tggccgaggt cctgagctgg cagttctcct ccaccaccaa gcgaggactg 1560
 agcatcgagc agctgactac actggcagag aaactcttgg gacctggtgt gaattattca 1620
 ggggtgtcaga tcacatgggc taaattttgc aaagaaaaca tggctggcaa gggcttctcc 1680
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 ttcaactggg tggagaagga catcagcggg aagaccaga tccagtccgt ggaaccatac 1920
 acaaagcagc agctgaacaa catgtcattt gctaaaatca tcatgggcta taagatcatg 1980
 gatgctacca atatcctggt gtctccactg gtctatctct atcctgacat tcccaaggag 2040

gaggcattcg gaaagtattg tcggccagag agccaggagc atcctgaagc tgaccaggt 2100
 agcgctgccc catacctgaa gaccaagttt atctgtgtga caccaacgac ctgcagcaat 2160
 accattgacc tgccgatgtc ccccgact ttagattcat tgatgcagtt tggaaataat 2220
 ggtgaagggtg ctgaaccctc agcaggaggg cagtttgagt cctcacctt tgacatggag 2280
 ttgacctcgg agtgcgctac ctcccccatg tga 2313

<210> 56

<211> 770

<212> PRT

<213> Homo sapiens

<220>

<221> STAT3 : Transcription factor

<222> (1)..(770)

<223>

<400> 56

Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr Leu Glu
 1 5 10 15

Gln Leu His Gln Leu Tyr Ser Asp Ser Phe Pro Met Glu Leu Arg Gln
 20 25 30

Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser
 35 40 45

Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile
 50 55 60

Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln
 65 70 75 80

His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu
 85 90 95

Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu
 100 105 110

Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln
115 120 125

Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu
130 135 140

Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu Glu Gln
145 150 155 160

Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe Asn Tyr
165 170 175

Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn
180 185 190

Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
195 200 205

Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
210 215 220

Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu
225 230 235 240

Ala Asp Trp Lys Arg Arg Gln Gln Ile Ala Cys Ile Gly Gly Pro Pro
245 250 255

Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu
260 265 270

Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln
275 280 285

Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met
290 295 300

Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala
305 310 315 320

Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro
325 330 335

Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu
340 345 350

Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile

355					360					365					
Asp	Lys	Asp	Ser	Gly	Asp	Val	Ala	Ala	Leu	Arg	Gly	Ser	Arg	Lys	Phe
370					375						380				
Asn	Ile	Leu	Gly	Thr	Asn	Thr	Lys	Val	Met	Asn	Met	Glu	Glu	Ser	Asn
385					390				395						400
Asn	Gly	Ser	Leu	Ser	Ala	Glu	Phe	Lys	His	Leu	Thr	Leu	Arg	Glu	Gln
				405				410						415	
Arg	Cys	Gly	Asn	Gly	Gly	Arg	Ala	Asn	Cys	Asp	Ala	Ser	Leu	Ile	Val
		420						425				430			
Thr	Glu	Glu	Leu	His	Leu	Ile	Thr	Phe	Glu	Thr	Glu	Val	Tyr	His	Gln
		435				440						445			
Gly	Leu	Lys	Ile	Asp	Leu	Glu	Thr	His	Ser	Leu	Pro	Val	Val	Val	Ile
450						455				460					
Ser	Asn	Ile	Cys	Gln	Met	Pro	Asn	Ala	Trp	Ala	Ser	Ile	Leu	Trp	Tyr
465				470						475				480	
Asn	Met	Leu	Thr	Asn	Asn	Pro	Lys	Asn	Val	Asn	Phe	Phe	Thr	Lys	Pro
				485				490						495	
Pro	Ile	Gly	Thr	Trp	Asp	Gln	Val	Ala	Glu	Val	Leu	Ser	Trp	Gln	Phe
		500						505				510			
Ser	Ser	Thr	Thr	Lys	Arg	Gly	Leu	Ser	Ile	Glu	Gln	Leu	Thr	Thr	Leu
		515				520						525			
Ala	Glu	Lys	Leu	Leu	Gly	Pro	Gly	Val	Asn	Tyr	Ser	Gly	Cys	Gln	Ile
530						535				540					
Thr	Trp	Ala	Lys	Phe	Cys	Lys	Glu	Asn	Met	Ala	Gly	Lys	Gly	Phe	Ser
545				550						555				560	
Phe	Trp	Val	Trp	Leu	Asp	Asn	Ile	Ile	Asp	Leu	Val	Lys	Lys	Tyr	Ile
				565				570						575	
Leu	Ala	Leu	Trp	Asn	Glu	Gly	Tyr	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu
		580						585				590			
Arg	Glu	Arg	Ala	Ile	Leu	Ser	Thr	Lys	Pro	Pro	Gly	Thr	Phe	Leu	Leu
		595				600						605			

<222> (1) .. (774)

<223> mCIS

<400> 57
atggtcctct gcgtacaggg atcttgtcct ttgctggctg tggagcaaat tgggcggcgg 60
cctctgtggg cccagtcctt ggagctgccc gggccagcca tgcagccctt acccactggg 120
gcattcccag aggaagtgc agaggagacc cctgtccagg cagagaatga accgaagggtg 180
ctagaccctg agggggatct gctgtgcata gccaaagacgt tctcctacct tcgggaatct 240
gggtggtact ggggttctat tacagccagc gaggcccggc agcacctaca gaagatgccg 300
gagggtacat tcctagtctg agacagcacc caccacagct acctgttcac actgtcagtc 360
aaaaccaccc gtggccccac caacgtgcgg atcgagtacg ccgattctag cttccggctg 420
gactctaact gcttgtcaag acctcgaatc ctggccttcc cagatgtggg cagccttgtg 480
cagcactatg tggcctcctg tgcagctgac acccgagcgg acagcccggg tcctgtctcc 540
acccagcccc tgcctatgtc taagcaagat gcacctagtg actcggtgct gcctatcccc 600
gtggctactg cagtgcacct gaaactgggt cagccctttg tgcgcaggag cagtgcccg 660
agcttacaac atctgtgtcg gctagtcac aaccgtctgg tggccgacgt ggactgctta 720
ccctgcccc ggcgtatggc cgactacctc cgacagtacc ccttccaact ctga 774

<210> 58

<211> 257

<212> PRT

<213> Homo sapiens

<220>

<221> mCIS

<222> (1) .. (257)

<223>

<400> 58

Met Val Leu Cys Val Gln Gly Ser Cys Pro Leu Leu Ala Val Glu Gln
1 5 10 15

Ile Gly Arg Arg Pro Leu Trp Ala Gln Ser Leu Glu Leu Pro Gly Pro

Leu

<210> 59
 <211> 639
 <212> DNA
 <213> Homo sapiens

<220>
 <221> gene
 <222> (1) .. (639)
 <223> mSOCS1

<400> 59
 atggttagcac gcaaccaggt ggcagccgac aatgcgatct ccccggcagc agagccccga 60
 cggcgggtcag agccctcctc gtccctcgtct tcgtcctcgc cagcggcccc cgtgcgtccc 120
 cggccctgcc cggcgggtccc agccccagcc cctggcgaca ctcaacttcg caacttcgcg 180
 tcccactccg attaccggcg catcacgcgg accagcgcgc tcctggacgc ctgcgggttc 240
 tattggggac ccctgagcgt gcacggggcg cagcagcggc tgcgtgccga gcccggtggg 300
 accttcttgg tgcgcgacag tcgccaacgg aactgcttct tcgcgctcag cgtgaagatg 360
 gcttcggggc ccacgagcat ccgcgtgcac ttccaggccg gccgcttcca cttggacggc 420
 agccgcgaga ctttcgactg ccttttcgag ctgctggagc actacgtggc ggcgcgcgcg 480
 cgcattgttg gggccccgct gcgccagcgc cgcgtgcggc cgtgcagga gctgtgtcgc 540
 cagcgcacgc tggccgccgt gggtcgcgag aacctggcgc gcacccctct taaccgggta 600
 ctccgtgact acctgagttc cttccccttc cagatctga 639

<210> 60
 <211> 212
 <212> PRT
 <213> Homo sapiens

<220>
 <221> mSOCS1

<223>

<400> 60

Pro Phe Gln Ile

210

<210> 61

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> linker sequence

<400> 61
gggccacgaa

10

<210> 62

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> linker sequence

<400> 62
ttcgtggccc ctg

13

<210> 63

<211> 138

<212> DNA

<213> Artificial Sequence

<220>

<223> pP6 vector sequence

<400> 63
ctagccatgg ccgcaggggc cgcggccgca ctagtgggga tccttaatta aagggccact
ggggcccccgt gtaccggcgt ccccgccgcc ggcgtgatca cccctaggaa ttaatttccc
ggtgaccccgt ggggagct

60

120

138

<210> 64

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> pB6 vector sequence (5'-3')

<400> 64
catggccgga cgggccgcgg ccgcactagt ggggatcctt aattaaagg ccactggggc 60
cccc 64

<210> 65

<211> 76

<212> DNA

<213> Artificial sequence

<220>

<223> pB20 vector sequence (5'-3')

<400> 65
aattcggggc cggacgggcc gcggccgcac tagtggggat ccttaattaa gggccactgg 60
ggcccctcga cctgca 76

<210> 66

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> primer

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